Additional file 3

Figure S1: Multiple sequence alignment of Smp1-Smp4 proteins from different *Schizosaccharomyces* species. Abbreviations: Sp, *S. pombe*; So, *S. octosporus*; Sj, *S. japonicus*; Sc, *S. cryophilus*. Homologues were identified by BLAST searching the UNIPROTKB_FUNGI database at the Universal Protein Resource (UniProt). Alignments were generated using Clustal Ω (1.2.4).

SpSmp1 SjSmp1	MSPRASLEKELNSARLLHATINAMDVYTQNLINELQEARDSINDLQRAHERLKLVGAKAKLQIKRDEKKPKS MQQHRKQQLKEAKMLHATVNAVDLYLSELLEDIRASSDAIKKLDTSENKFENTLSQAIKKTGKNA : :::*: *: **: *: *: *: *: *: *: *: *: *	72 65
SpSmp2	MQHNKENHFVEDAKQFQEKAKLYQGNYYTLDGELITIIPSSKEGFRSCKSLYYKKKQPIPGR	62
ScSmp2	MEODKENOLNLPKLSIPODIKVFOGNYYTLDGEOTP-NPDGTTEFKTCKALYYKSKKPIPGR	61
1	*:::***::	
SpSmp3	MAQTFQEKQQSRRIKMSTGNFFSRMWNAVVFGFGAAIGASVANAALGACCG-	51
SjSmp3	MATFQEKQGQRRIKMRTGNFFSRMWNAVIFGFGAAIGATVANAALGACCG-	50
ScSmp3	MGRTFQEKQQSRRVKMSTGNIFSRVWNSVVFGFGAALGATAASAMIGACCG-	51
SoSmp3	MARTFQEKQQGRRMKMSTGNIFSRVWNSVVFGFGAALGATAASAMLGACCGG	52
-	***** ** ** *** *** *** *** ** * * * * *	
SpSmp4	MSAPYKNLDRDTKHTHPKLNETERNLNRGWGDVKKEELYEDLAQSDADKQLAEDKMETKYEKSKPAPSD	69
SoSmp4	MSPAPYKDLSKDTVHTHPPIHESERREEHGWGSLKKEPLMEDQAEQDAKADLSKDKKEVKEEASRPPPSV	70
ScSmp4	MSPAPYKDLSKDTVHTHPAIRESERREQHGWGDLNKEPLMEDQAERDAKNDLSKDQKEVKEQASRPAPNN	70
SjSmp4	MPYMPOVKHGEVIRDDRHSHTGLKISDRADTRGWGDVKHEREFEELAERDAETDORRDTEEVOKEPELLPPO-	72
J 1	. : :: :* *:* :: :* :***.:::* *: *: ** : . * *.: : . *.	

Figure S2: Phenotypic analysis of $smp1\Delta$ - $smp4\Delta$ cells. **A.** Microscopic images of wild-type, $smp1\Delta$, $smp2\Delta$, $smp3\Delta$ and $smp4\Delta$ cells growing exponentially in YE4S medium at 32°C. Scale bar: 10 μm. **B.** Growth rates (OD_{600nm} versus time) of wild-type (WT), $smp1\Delta$, $smp2\Delta$, $smp3\Delta$ and $smp4\Delta$ cells growing in YE4S medium at 32°C. **C.** Examples of meiotic asci formed by self-crossing wild-type, $smp1\Delta$, $smp2\Delta$, $smp3\Delta$ and $smp4\Delta$ strains of opposite mating type on SPA agar at 25°C for 48 hours. The figure was assembled from multiple representative images of the same crosses. Scale bar: 10 μm.

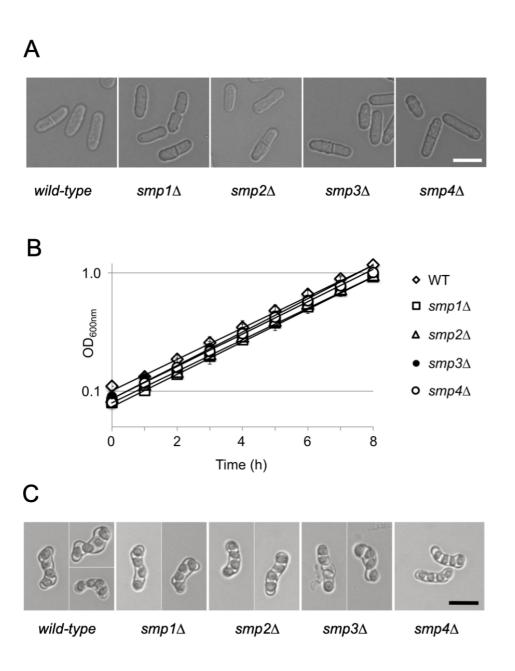


Figure S3: Insertion sites relative to sgRNA and PAM sequences. Sequences of *smp1-S1 – smp1-S3* and *smp1-S1 – smp3-S3* alleles are shown. PAM sequences are shown in bold, sequence corresponding to sgRNA in red. Note that the insertion in *smp-S3* also deletes two nucleotides. See Table S6 for identity of inserted *Oncorhynchus* sequences.

sgRNA **ACGATTTACAGAGTAAGTAACGG**GTACATTGAAGATTGC smp1 smp1-S1ACGATTTACAGAGTAAGT---384---AACGGGTACATTGAAGATTGC ACGATTTACAGAGTAAGT---183---AACGGGTACATTGAAGATTGC smp1-S2smp1-S3ACGATTTACAGAGTAA-----73---AACGGGTACATTGAAGATTGC inserted PAM sequences (bp) sgRNA smp3 CGCACCGAAGCCGAACACGACGGCATTCCACATTCTAGA smp3-S1CGCACCGAAGCCGAAC---121---ACGACGCATTCCACATTCTAGA smp3-S2CGCACCGAAGCCGAAC---121---ACGACGCATTCCACATTCTAGA smp3-S3CGCACCGAAGCCGAAC---113---ACGACGGCATTCCACATTCTAGA inserted PAM sequences (bp)